

A COMPARE OF THE PHYLOGENETIC RECONSTRUCTIONS SEQUENCE RESULTS IN THE PROGRAM MEGA 5 AND THE MATLAB PACKAGE

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The aim of the research was to compare the results of phylogenetic analysis of the nucleotide sequences of 16S RNA strains *Acidobacillus ferrooxidans*, which was made by the programs Mega 5 and MatLab.

We used annotated in GenBank database sequences in the work. The conservative sequences were chosen for increasing the reliability level of the findings. It allowed to analyze not a genetic diversity, but a result of accuracy of the realization calculations.

The tasks of the research were to compare the results of phylogenetic reconstruction of the sequence depending on the chosen evolutionary model; one-parameter model of Jukes-Cantor and Kimura's two-parameter model, the three-parameter model of Tamura.

Using the Mega 5 gives an advantage to carry out such an analysis, because it allows you to use more statistical methods. The MATLAB package program basically reconstructs phylogeny, focusing on methods of analyzing genetic distance, but gives you the opportunity for a wide bioinformatics analysis of the sequences themselves.

By analyzing the topology of the derived phylogenetic trees, we noted, that all sequences had formed two separate global clusters, irrespective of chosen evolution model. It registered the biggest difference in the resulting topology when using the Maximum Parsimony (Mega 5) method. The differences in the forming of the internal nodes confidence level were minimal.

When using packet MatLab, tree topology was similar tree topology derived when using Mega 5 for each evolutionary model.

It should be noted, the topologies graphics realization constructed tree in MatLab package is more vivid. It makes easier visual perception. However, the package MatLab, more exacting to the data and in the case of a significant discrepancy between the lengths of the sequences the analysis becomes difficult or impossible.

Comparison of the results showed the possibility of simultaneous use of both programs when working with the sequences without the risk of serious errors, due to mismatch of algorithms.